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**Amendment to the Specification**

Please replace the paragraph starting at page 21, line 1 to line 26 with the following paragraph:

Figures 9A-9B. Structure of *IRTA1* and *IRTA2* cDNAs. Figs. 9A, 9B) Schematic representation of the full-length *IRTA1* (Fig. 9A) and *IRTA2* (Fig. 9B) cDNAs. Pattern filled, wide boxes represent coding domains and narrow boxes represent untranslated regions (UTR). The predicted site for signal peptidase cleavage is marked by an arrowhead and ~~was derived according to the signal IP World Wide Web server at <http://www.cbs.dtu.dk/service/SignalIP>~~. The transmembrane domain prediction algorithm is described in Tusnady et al, 1998. SP, signal peptide; EC, extracellular domain; Ig, immunoglobulin-type; TM, transmembrane domain; CYT, cytoplasmic domain; A(n), polyA tail, GPI, glycosylphosphatidyl inositol. In (Fig. 9A), arrows in the 3' UTR indicate different polyadenylation addition sites utilized in the *IRTA1* cDNA. In (Fig. 9B), different 3'UTR regions in *IRTA2* isoforms are differentially shaded. Bars underneath the UTR regions in (Fig. 9A) and (Fig. 9B) identify probes used for Northern blot analysis in Fig. 12.